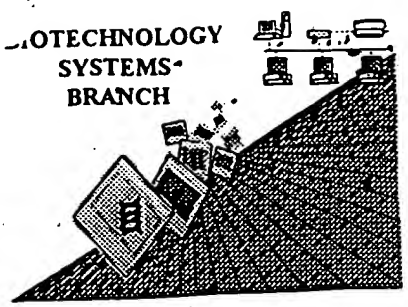
0590
10

BIOTECHNOLOGY SYSTEMS BRANCH



RAW SEQUENCE LISTING ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 09/816669

Source: OIPE

Date Processed by STIC: 10/04/01

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.
PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

1) **INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,**
2) **TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY**

FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.
PATENTIN 2.1 e-mail help: patin21help@uspto.gov or phone 703-306-4119 (R. Wax)
PATENTIN 3.0 e-mail help: patin3help@uspto.gov or phone 703-306-4119 (R. Wax)

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 3.0 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW:

Checker Version 3.0

The Checker Version 3.0 application is a state-of the-art Windows based software program employing a logical and intuitive user-interface to check whether a sequence listing is in compliance with format and content rules. Checker Version 3.0 works for sequence listings generated for the original version of 37 CFR §§1.821 – 1.825 effective October 1, 1990 (old rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual Property Organization (WIPO) Standard ST.25.
Checker Version 3.0 replaces the previous DOS-based version of Checker, and is Y2K-compliant. Checker allows public users to check sequence listings in Computer Readable form (CRF) before submitting them to the United States Patent and Trademark Office (USPTO). Use of Checker prior to filing the sequence listing is expected to result in fewer errored sequence listings, thus saving time and money.

Checker Version 3.0 can be down loaded from the USPTO website at the following address:

http://www.uspto.gov/web/offices/pac/checker

Raw Sequence Listing Error Summary

ERROR DETECTED	SUGGESTED CORRECTION	SERIAL NUMBER: 09/816669

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO

1	Wrapped Nucleics Wrapped Aminos	The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."
2	Invalid Line Length	The rules require that a line not exceed 72 characters in length. This includes white spaces.
3	Misaligned Amino Numbering	The numbering under each 5th amino acid is misaligned. Do not use tab codes between numbers; use space characters, instead.
4	Non-ASCII	The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.
5	Variable Length	Sequence(s)____contain n's or Xaa's representing more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.
6	PatentIn 2.0 "bug"	A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s) _____. Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.
7	Skipped Sequences (OLD RULES)	Sequence(s) _____ missing. If intentional, please insert the following lines for each skipped sequence: (2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown) (i) SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading) (xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown) This sequence is intentionally skipped Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.
8	Skipped Sequences (NEW RULES)	Sequence(s) _____ missing. If intentional, please insert the following lines for each skipped sequence <210> sequence id number <400> sequence id number 000
9	✓ Use of n's or Xaa's (NEW RULES)	Use of n's and/or Xaa's have been detected in the Sequence Listing. Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present. In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.
10	Invalid <213> Response	Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown o is Artificial Sequence
11	Use of <220>	Sequence(s) _____ missing the <220> "Feature" and associated numeric identifiers and responses. Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section. (See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules)
12	PatentIn 2.0 "bug"	Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.
13	Misuse of n	n can only be used to represent a single nucleotide in a nucleic acid sequence. N is not used to represen any value not specifically a nucleotide.

AMC/MH – Biotechnology Systems Branch – 08/21/2001

may

The type of errors shown exist throughout the Sequence Listing. Please check subsequent sequences for similar errors.

OIPE

RAW SEQUENCE LISTING DATE: 10/04/2001
PATENT APPLICATION: US/09/816,669 TIME: 17:20:41

Input Set : A:\PTO_VSK.txt
Output Set: N:\CRF3\10042001\I816669.raw

3 <110> APPLICANT: GARABEDIAN, Michael
4 TANEJA, Samir
5 HITTELMAN, Adam
6 MARKUS, Steven
8 <120> TITLE OF INVENTION: METHOD FOR SCREENING TRANSCRIPTIONAL COREGULATORY PROTEINS OF
9 TRANSCRIPTION FACTORS, AND ANDROGEN RECEPTOR TRANSCRIPTIONAL COREGULATORY
10 PROTEINS AS TARGETS FOR ANDROGEN RECEPTOR-DEPENDENT DISEASES
12 <130> FILE REFERENCE: GARABEDIAN=1.1A
C--> 14 <140> CURRENT APPLICATION NUMBER: US/09/816,669
15 <141> CURRENT FILING DATE: 2001-03-26
17 <150> PRIOR APPLICATION NUMBER: 60/225,618
18 <151> PRIOR FILING DATE: 2000-08-15
20 <150> PRIOR APPLICATION NUMBER: 60/191,768
21 <151> PRIOR FILING DATE: 2000-03-24
23 <160> NUMBER OF SEQ ID NOS: 20
25 <170> SOFTWARE: PatentIn version 3.0
27 <210> SEQ ID NO: 1
28 <211> LENGTH: 474
29 <212> TYPE: DNA
30 <213> ORGANISM: human
32 <400> SEQUENCE: 1
33 atggcgacgc cccctaagcg gcgggcggtg gaggccacgg gggagaaagt gctgcgctac 60
35 gagaccttca tcagtgacgt gctgcagcgg gacttgcgaa aggtgctgga ccatcgagac 120
37 aaggtatatg agcagctggc caaatacctt caactgagaa atgtcattga gcgactccag 180
39 gaagctaagc actcggagtt atatatgcag gtggatttgg gctgtaactt cttcgttgac 240
41 acagtggtcc cagatacttc acgcatctat gtggccctgg gatatggttt tttcctggag 300
43 ttgacactgg cagaagctct caagttcatt gatcgtaaga gctctctcct cacagagctc 360
45 agcaacagcc tcaccaagga ctccatgaat atcaaagccc atatccacat gttgctagag 420
47 gggcttagag aactacaagg cctgcagaat ttcccagaga agcctcacca ttga 474
50 <210> SEQ ID NO: 2
51 <211> LENGTH: 157
52 <212> TYPE: PRT
53 <213> ORGANISM: human
55 <400> SEQUENCE: 2
57 Met Ala Thr Pro Pro Lys Arg Arg Ala Val Glu Ala Thr Gly Glu Lys
58 1 5 10 15
60 Val Leu Arg Tyr Glu Thr Phe Ile Ser Asp Val Leu Gln Arg Asp Leu
61 20 25 30
63 Arg Lys Val Leu Asp His Arg Asp Lys Val Tyr Glu Gln Leu Ala Lys
64 35 40 45
66 Tyr Leu Gln Leu Arg Asn Val Ile Glu Arg Leu Gln Glu Ala Lys His
67 50 55 60
69 Ser Glu Leu Tyr Met Gln Val Asp Leu Gly Cys Asn Phe Phe Val Asp
70 65 70 75 80
72 Thr Val Val Pro Asp Thr Ser Arg Ile Tyr Val Ala Leu Gly Tyr Gly
73 85 90 95
75 Phe Phe Leu Glu Leu Thr Leu Ala Glu Ala Leu Lys Phe Ile Asp Arg

1 Does Not Comply
Corrected Diskette Needed
Errored: See pages 4 and 5 and Error Summary Sheet

RAW SEQUENCE LISTING DATE: 10/04/2001
PATENT APPLICATION: US/09/816,669 TIME: 17:20:41

Input Set : A:\PTO_VSK.txt
Output Set: N:\CRF3\10042001\I816669.raw

```
76              100                 105                 110
78 Lys Ser Ser Leu Leu Thr Glu Leu Ser Asn Ser Leu Thr Lys Asp Ser
79          115                 120                 125
81 Met Asn Ile Lys Ala His Ile His Met Leu Leu Glu Gly Leu Arg Glu
82      130                 135                 140
84 Leu Gln Gly Leu Gln Asn Phe Pro Glu Lys Pro His His
85 145                 150                 155
87 <210> SEQ ID NO: 3
88 <211> LENGTH: 1097
89 <212> TYPE: DNA
90 <213> ORGANISM: human
92 <400> SEQUENCE: 3
93 aaatgcacaa cccggacgga agtgcctctc cgacagcaga tccaggctcg gagctccaga     60
95 cgctgggaca ggccgcccgc agaccacccc cgccgcgcgc gggacacgac gccccccgca    120
97 ggacacgccc atcagcccgg aaacccctga gctgcttctc ccggaggccg atgcccaccc    180
99 gggagccccc aaagactcgc ggctcccggg ggcacctgca tactcacccg cctgggcctg    240
101 ggcccccgct gcagggactg gcgccccgag gcctcaaaac cagcgccccc cgccctccgt    300
103 gccagcccca gccgggaccc cacaaggcaa agaccaagaa gattgtgttt gaggatgagt    360
105 tgctctccca ggccctcctg ggcgccaaga agcctattgg agccatccct aaggggcata    420
107 agcctaggcc ccacccagtg cccgactatg agcttaagta cccgccagtg agcagtgaga    480
109 gggaacggag ccgctatgtc gcagtgttcc aggaccagta cggagagttc ttggagctcc    540
111 agcacgaggt ggggtgtgca caggcaaagc tcaggcagct ggaggccctg ctgagctccc    600
113 tgcccccacc ccaaagccag aaggaggccc aagttgcagc ccgggtttgg agggagtttg    660
115 agatgaagcg aatggatcct ggcttcctgg acaagcaggc tcgctgccac tacctgaagg    720
117 gtaaactgag gcatctcaag actcagatcc agaaattcga tgaccaagga gacagcgagg    780
119 gctccgtgta cttctaagtg cccctgcaga tgggcagagg gatgcatggg gatgcaggtc    840
121 ccttgcattt cttggtatct ctcagctttt cctcttgcag ctccccctac caggggtcgc    900
123 tttctcctgg attgcaaatg cctcttcagt ttggactcag ctctgacagc ccctcctcca    960
125 ggaaggcctt ccaggacttc ctcctctggg tcctctagct ctgaccctac agggactcca   1020
127 gatctcaacc tgttccctgg aagtagggcc tgctctccat cccagtgaaa taaacatgta   1080
129 ttagacacct aaaaaaa                                                 1097
132 <210> SEQ ID NO: 4
133 <211> LENGTH: 264
134 <212> TYPE: PRT
135 <213> ORGANISM: Human
137 <400> SEQUENCE: 4
139 Met His Asn Pro Asp Gly Ser Ala Ser Pro Thr Ala Asp Pro Gly Ser
140 1               5                  10                  15
142 Glu Leu Gln Thr Leu Gly Gln Ala Ala Arg Arg Pro Pro Pro Pro Arg
143             20                  25                  30
145 Ala Gly His Asp Ala Pro Arg Arg Thr Arg Pro Ser Ala Arg Lys Pro
146         35                  40                  45
148 Leu Ser Cys Phe Ser Arg Arg Pro Met Pro Thr Arg Glu Pro Pro Lys
149     50                  55                  60
151 Thr Arg Gly Ser Arg Gly His Leu His Thr His Pro Pro Gly Pro Gly
152 65                  70                  75                  80
154 Pro Pro Leu Gln Gly Leu Ala Pro Arg Gly Leu Lys Thr Ser Ala Pro
155                 85                  90                  95
157 Arg Pro Pro Cys Gln Pro Gln Pro Gly Pro His Lys Ala Lys Thr Lys
```

RAW SEQUENCE LISTING DATE: 10/04/2001
PATENT APPLICATION: US/09/816,669 TIME: 17:20:41

Input Set : A:\PTO_VSK.txt
Output Set: N:\CRF3\10042001\I816669.raw

```
158             100                 105                 110
160 Lys Ile Val Phe Glu Asp Glu Leu Leu Ser Gln Ala Leu Leu Gly Ala
161         115                 120                 125
163 Lys Lys Pro Ile Gly Ala Ile Pro Lys Gly His Lys Pro Arg Pro His
164     130                 135                 140
166 Pro Val Pro Asp Tyr Glu Leu Lys Tyr Pro Pro Val Ser Ser Glu Arg
167 145                 150                 155                 160
169 Glu Arg Ser Arg Tyr Val Ala Val Phe Gln Asp Gln Tyr Gly Glu Phe
170                 165                 170                 175
172 Leu Glu Leu Gln His Glu Val Gly Cys Ala Gln Ala Lys Leu Arg Gln
173             180                 185                 190
175 Leu Glu Ala Leu Leu Ser Ser Leu Pro Pro Pro Gln Ser Gln Lys Glu
176         195                 200                 205
178 Ala Gln Val Ala Ala Arg Val Trp Arg Glu Phe Glu Met Lys Arg Met
179     210                 215                 220
181 Asp Pro Gly Phe Leu Asp Lys Gln Ala Arg Cys His Tyr Leu Lys Gly
182 225                 230                 235                 240
184 Lys Leu Arg His Leu Lys Thr Gln Ile Gln Lys Phe Asp Asp Gln Gly
185                 245                 250                 255
187 Asp Ser Glu Gly Ser Val Tyr Phe
188             260
190 <210> SEQ ID NO: 5
191 <211> LENGTH: 517
192 <212> TYPE: DNA
193 <213> ORGANISM: Human
195 <220> FEATURE:
196 <221> NAME/KEY: misc_feature
197 <223> OTHER INFORMATION: n at position 65 is unknown. ~~poor~~ good
200 <400> SEQUENCE: 5
201 gaacggcacg agggcgcgcc acgcgcggga agcggcgcgc ggagcgcgcg cggcgggccg     60
W--> 203 cgcangcgag ggagccgagc gcccgmacgc gcccgagcgg acasacgcca gagccgcgcc    120
205 ccgggccgag cgcagcgcgc cggccgssyg ggccgccagg ggcgcgcgcg gcggagcgcg    180
207 gggcgcgmga aaaggggccc ggcggagacc aagggcaggc gcggcccgca agggcgccgg    240
209 ggaaggcgcc cggcaaggag gcggacaagc ggagcaggcc aacgagacgc gcgcacccac    300
211 acacgagcgc gagccgccac aacaccacac ccggcccaag gagaacagca cgccaacgcg    360
213 ccagycacgg cgggcacggg aggcgggcca cacacagcgg ccccgccaag gcacggcgca    420
215 cggcacaagg gcaccacgcc agacaagcga ggaggcagca cgccgagacc ggccggaggg    480
217 ccgcgaccgc cggagaaaag gaacagagag cccccca                            517
220 <210> SEQ ID NO: 6
221 <211> LENGTH: 189
222 <212> TYPE: PRT
223 <213> ORGANISM: Human
225 <400> SEQUENCE: 6
227 Glu Phe Gly Thr Arg Ala Arg Phe Thr Arg Gly Lys Ser Ala Leu Leu
228 1               5                   10                  15
230 Glu Arg Ala Leu Ala Arg Pro Arg Thr Glu Val Ser Leu Ser Ala Phe
231             20                  25                  30
233 Ala Leu Leu Ser Pro Ser Trp Tyr Ser Thr Ala Arg Ala Val Phe Ser
234         35                  40                  45
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RAW SEQUENCE LISTING DATE: 10/04/2001
PATENT APPLICATION: US/09/816,669 TIME: 17:20:41

Input Set : A:\PTO_VSK.txt
Output Set: N:\CRF3\10042001\I816669.raw

```
236 Val Ala Glu Leu Gln Ser Arg Leu Ala Ala Leu Gly Arg Gln Val Gly
237     50                  55                  60
239 Ala Arg Val Leu Asp Ala Leu Val Ala Arg Glu Lys Gly Ala Arg Arg
240 65                  70                  75                  80
242 Glu Thr Lys Val Leu Gly Ala Leu Leu Phe Val Lys Gly Ala Val Trp
243                 85                  90                  95
245 Lys Ala Leu Phe Gly Lys Glu Ala Asp Lys Leu Glu Gln Ala Asn Asp
246             100                 105                 110
248 Asp Ala Arg Thr Phe Tyr Ile Ile Glu Arg Glu Pro Leu Ile Asn Thr
249         115                 120                 125
251 Tyr Ile Ser Val Pro Lys Glu Asn Ser Thr Leu Asn Cys Ala Ser Phe
252     130                 135                 140
254 Thr Ala Gly Ile Val Glu Ala Val Leu Thr His Ser Gly Phe Pro Ala
255 145                 150                 155                 160
257 Lys Val Thr Ala His Trp His Lys Gly Thr Thr Leu Met Ile Lys Phe
258                 165                 170                 175
260 Glu Glu Ala Val Ile Ala Arg Asp Arg Leu Glu Gly Arg
261             180                 185
263 <210> SEQ ID NO: 7
264 <211> LENGTH: 126
265 <212> TYPE: DNA
266 <213> ORGANISM: Human
268 <400> SEQUENCE: 7
269 gaattcggca cgaggctcaa gccctacgtg agctacctcg cccctgagag cgaggagacg     60
271 cccctgacgg ccgcgcagct cttcagcaag ccgttggcgc cttgccatcg aaaaggactt    120
273 caagga                                                             126
276 <210> SEQ ID NO: 8
277 <211> LENGTH: 42
278 <212> TYPE: PRT
279 <213> ORGANISM: Human
281 <400> SEQUENCE: 8
283 Glu Phe Gly Thr Arg Leu Lys Pro Tyr Val Ser Tyr Leu Ala Pro Glu
284 1               5                   10                  15
286 Ser Glu Glu Thr Pro Leu Thr Ala Ala Gln Leu Phe Ser Lys Pro Leu
287             20                  25                  30
289 Ala Pro Cys His Arg Lys Gly Leu Gln Gly
290         35                  40
292 <210> SEQ ID NO: 9
293 <211> LENGTH: 678
294 <212> TYPE: DNA
295 <213> ORGANISM: Human
297 <220> FEATURE:
298 <221> NAME/KEY: misc_feature
299 <223> OTHER INFORMATION: n at position 651 is unknown.
302 <400> SEQUENCE: 9
303 gaattcggca cgaggattca ttgcccccac aatcctaggc ctacccgccg cagtactgat     60
305 cattctattt ccccctctat tgatccccac ctccaaatat ctcatcaaca accgactaat    120
307 caccacccaa caatgactaa tcaaactaac ctcaaaacaa atgataacca tacacaacac    180
309 taaaggacga acctgatctc ttatactagt atccttaatc atttttattg ccacaactaa    240
```

Errored — need to include reference to position 657.

The type of errors shown exist throughout the Sequence Listing. Please check subsequent sequences for similar errors.

RAW SEQUENCE LISTING DATE: 10/04/2001
PATENT APPLICATION: US/09/816,669 TIME: 17:20:42

Input Set : A:\PTO_VSK.txt
Output Set: N:\CRF3\10042001\I816669.raw

311 cctcctcgga ctcctgcctc actcatttac accaaccacc caactatcta taaacctagc 300
313 catggccatc cccttatgag cgggcgcagt gattataggc tttcgctcta agattaaaaa 360
315 tgccctagcc cacttcttac cacaaggcac acctacaccc cttatcccca tactagttat 420
317 tatcgaaacc atcagcctac tcattcaacc aatagccctg gccgtacgcc taaccgctaa 480
319 cattactgca ggccacctac tcatgcacct aattggaagc gccaccctag caatatcaac 540
321 cattaacctt cctctacact tatcatcttc acaattctaa ttctactgac tatcctagaa 600
W--> 323 atcgctgtcg ccttaatcca agcctacgtt ttcacacttc tagtaagcct ntactgnacg 660
325 acaacacata aaaaaaaa 678
328 <210> SEQ ID NO: 10
329 <211> LENGTH: 60
330 <212> TYPE: PRT
331 <213> ORGANISM: Human
333 <400> SEQUENCE: 10
335 Glu Phe Gly Thr Arg Ile His Cys Pro His Asn Pro Arg Pro Thr Arg
336 1 5 10 15
338 Arg Ser Thr Asp His Ser Ile Ser Pro Ser Ile Asp Pro His Leu Gln
339 20 25 30
341 Ile Ser His Gln Gln Pro Thr Asn His His Pro Thr Met Thr Asn Gln
342 35 40 45
344 Thr Asn Leu Lys Thr Asn Asp Asn His Thr Gln His
345 50 55 60
347 <210> SEQ ID NO: 11
348 <211> LENGTH: 1918
349 <212> TYPE: DNA
350 <213> ORGANISM: Human
352 <400> SEQUENCE: 11
353 gaattccaat gtggtaaagt cttcgctcaa acatcacaac ttgcaaggca ttggagagtt 60
355 catactggag aaaaacctta caagtgtaat gactgtggca gagcctttag tgatcgttca 120
357 agcctaactt ttcatcaggc aatacatact ggagagaaac cttacaaatg tcatgaatgc 180
359 ggcaaggttt ttaggcacaa ttcatacctt gcaactcatc ggcgaattca tactggagag 240
361 aaaccttaca agtgtaatga gtgtgggaaa gcctttagta tgcattcaaa cctaactacc 300
363 cataaggtca tccatactgg agagaagcct tacaaatgta atcaatgtgg caaggtcttc 360
365 actcagaact cacaccttgc aaatcatcaa aggactcaca ccggagagaa accttaccga 420
367 tgcaatgagt gtgggaaagc cttcagtgtt cgttcaagcc taaccaccca tcaggcaatc 480
369 catactggga aaaaacctta caaatgtaat gaatgtggca aggtctttac tcaaaatgct 540
371 cacctggcaa atcaccgaag aattcatact ggggagaaac cttacaggtg tacagagtgt 600
373 gggaaagcct ttagggtaag atcaagtcta actacccata tggcaatcca cactggagaa 660
375 aagcgttaca aatgtaatga gtgtggcaag gtcttcaggc agagttcaaa tcttgcaagt 720
377 catcacagaa tgcataccgg agagaaacct tacaaatgag tgtggtgagg tcattaggta 780
379 caattcactc ctttcacatc agttaatttc attcttgaca gaatccttac aaatgtagtg 840
381 acagtggcca atccctcatg agttgaagca ttaatagata tgagaggcca taagcaagag 900
383 acatcatgta aacatatgtg gcagagggtc tatccaggcc tcgcaggtta ctaggcatca 960
385 agatttatat ctttgatgaa acgaaacaaa tgtaatatgc atcctgaggc cattacccag 1020
387 tgaccgatgg taagtgagga ttcctaggag gaataacagt ctctggtttc cctgtttgcc 1080
389 tttgatatta tacactgtag aatactcaca agtccaaata tgctaaaaat tatatatttt 1140
391 taactcacat acgaaaaggt tgcaggatat ttgtaggcag tcagttacct tcaccttatg 1200
393 aaatgtttca ctgagttatt tgaggttttt tggaaagcct actattgcgt ttcaatgtga 1260
395 actttgaaat cttattgtgc atccttacac accttccatg gtgctttctt ggaaagatca 1320
397 ttgggatgga aggatcattg attgggtgaa gatcattgat taggtgaagg attatttcta 1380

Errored: Unknown at location 657 is not identified in fields 221 or 223.

FYI: "Artificial Sequence" is the preferred field 213 term as opposed to "Artificial".

VERIFICATION SUMMARY DATE: 10/04/2001
PATENT APPLICATION: US/09/816,669 TIME: 17:20:43

Input Set : A:\PTO_VSK.txt
Output Set: N:\CRF3\10042001\I816669.raw

L:14 M:270 C: Current Application Number differs, Replaced Current Application Number
L:203 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:5
L:203 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5
L:323 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:9
L:323 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:9
L:1324 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:15
L:1336 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:16
L:1348 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:17
L:1360 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:18
L:1372 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:19
L:1384 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:20